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# Knowing the Biosphere: Documentation, Specimens, Archives, and Names Reveal Environmental Change and Emerging Pathogens

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## Abstract

One Health programs and trajectories are now the apparent standard for exploring the occurrence and distribution of emerging pathogens and disease. By definition, One Health has been characterized as a broadly inclusive, collaborative, and transdisciplinary approach with connectivity across local to global scales, which integrates the medical and veterinary community to recognize health outcomes emerging at the environmental nexus for people, animals, plants, and their shared landscapes. One Health has been an incomplete model, conceptually and operationally, focused on reactive and response-based foundations, to limit the impact of emerging pathogens and emerging infectious diseases and, as such, lacks a powerful proactive capacity. A proactive, predictive One Health is necessary, emanating in part from geographically/taxonomically broad and temporally deep biological collections of pathogen-host assemblages. The DAMA protocol (Document, Assess, Monitor, Act), the operational extension of the Stockholm paradigm (SP), accomplishes this task by encompassing holistic and strategic biological sampling of reservoir host assemblages and pathogens at environmental interfaces and more extensively through resurveys, with development of informatics resources digitally linked to physical specimens held in publicly accessible museum biorepositories. Archives of specimens are the foundations for accumulating interrelated archives of information (the baselines against which change can be identified and tracked), with collections serving as fundamental resources for biodiversity informatics under the conceptual evolutionary and ecological umbrella of the SP. A cultural and conceptual transformation is essential among the diverse practitioners in the One Health community, one that recognizes the necessity of placing pathogens in an evolutionary, ecological, and environmental context by integrating specimens and associated informatics into an infrastructure and networks for actionable information. As a community, it is essential to abandon response-based business as usual while looking forward toward proactive transboundary approaches that maximize our conceptual and taxonomic view of diversity across interconnected planetary scales that influence the complexity of pathogen-host interfaces. Evolution, where the past always influences the present and the future, defines our trajectory, as the need for sustained archives that describe the biosphere becomes more acute with each passing day.

**Keywords:** Stockholm paradigm, DAMA protocol, biorepositories, specimens and archives, pathogens, hosts and emerging disease, One Health

*Saving biodiversity and promoting human socioeconomic development is a complex issue that requires networks of both people and research programs. Networks require a common language and discourse, as well as collaborative development of theory and research programs. Modern systematists are the masters of a language powerful enough to facilitate such necessary discourse.*

Brooks and Hoberg, 2001

*In the absence of taxonomic names there is no information. With the wrong names there is incorrect information. Both situations emphasize consequences for how we identify and understand dynamic change for pathogen-host assemblages under a regime of climate warming.*

Brooks and Hoberg, 2007, 2013

## A Fundamental Context for Names

In the absence of organismal names, we are rudderless, lacking direction, wayward wanderers on an open sea of biodiversity with nothing but opinions in a vacuum. Names provide not only a safe harbor to anchor biodiversity sciences but are also the critical links for connectivity across environments, among organisms, and for transboundary explorations that allow us to make sense of a complex world that is experiencing accelerating change and transformation. Names link history to the present and can serve as a roadmap to the future. Across the history of humanity, original common and local names for animals and plants were later codified and classified in attempts to characterize life under the umbrella of science. The contemporary purveyors of names, or nomenclature in biology, are the systematists and taxonomists, who serve to bring a sense of phylogenetic order to the myriad of animals and plants, fungi, protists, eubacteria, and archaeobacteria that have populated the planet across Earth's history in the 6 kingdoms comprising the tree of life (e.g., Woese et al., 1990); despite the pervasive nature of viruses and perhaps prions, their placement within this hierarchy remains unresolved. Taxonomy, anchored in scientific collections, is the international language of biological diversity, establishing the framework necessary for scientific collaboration, cooperation, and the potential for clear communication. Biological specimens, the basis of museum archives in the era of digital biological heritage, facilitate opportunities for global metasynthesis of biodiversity and rigorous investigation of the biosphere. Specimens are the essential cornerstones for taxonomy as they validate names

and validate our theoretical view of the world. Understanding specimens is understanding evolution, where the past always influences the present and the future (e.g., Agosta and Brooks, 2020; Agosta, 2022). An evolutionary perspective, revealing history and structure of global diversity in accelerating change, defines our need for sustained archives, which becomes more acute with each passing day.

The *truth of a name* resides in a connection to organisms: the rich, persistent, and prolific soup of diversity ranging from the infinitesimally small viruses and microbes, to macroparasites, fungi, forest giants, and whales. As an extended community in science, we reveal and discover connectivity across this extraordinary mosaic assembled in space and time, the culmination of more than 600 million years for evolution of complex multicellular life on our planet. We explore and discover in ways familiar to all people—what we can see, touch, feel, sample, observe, and describe. A cumulative understanding of the biosphere emerges from human curiosity and discourse. A need to understand our surroundings has been continually refined since the earliest stories were passed around caves and fire rings millennia ago, through traditions of local knowledge, to the nuances of molecular pathways revealed in countless laboratories around the globe.

A fundamental necessity for ancestral hominins across Africa and Eurasia was the ability to know the biosphere, to distinguish suitable resources from potential danger. What could we consume; where and when could these plants and animals be procured; when were these safe and when were they deadly, potentially leading to the demise of you, your family, your tribe? These were the rudiments of natural history, with common names for plants, fungi, invertebrates, and vertebrates on land, shore, and sea, defining the local cornucopia for survival and persistence on landscapes under episodic and dynamic change. Natural histories broadened as modern humans expanded, coming to occupy nearly all habitats and landforms. A superlative story of ecological fitting is apparent (see Janzen, 1985; Agosta and Brooks, 2020) as our ancestors ebbed and flowed in environments, dispersing across landscapes to regions and continents. We will never know all the names in the biodiversity lexicons that accompanied 300,000 years of human dispersal and migration from Africa to Eurasia and Australia, to Oceania and Micronesia, to North America and through the South American tropics to the Tierra del Fuego. There are remarkable perceptions of the world captured in language—like the word that survives among the Inuit of Chukotka, Russia, that describes the sound and thundering presence of mammoths moving on the tundra-steppes of Beringia 20,000 years in the past (Payer et al., 2013).

*When there is an earthquake, we say that the mammoth are running. We even have a word for this, holgot.*

Related by Vyacheslav Shadrin, Yukaghir  
Council of Elders, Kolyma River Basin, Russia  
(Mustonen, 2009 in Payer et al., 2013)

An inclusive natural history and formalized taxonomy, or a common language, however, had to wait for the written record, as observations and memories are mutable and communication could be confused culturally over distances and time. A philosophical or pragmatic approach to characterizing the biosphere had been informal, with roots extending to the patterns of identifying and locating basic food and other resources (Berlin, 1992). Initially functional, developing taxonomies emphasized commonality of habitats such as all the fish and marine mammals in the sea combined as an inclusive group and only later refined in the context of essential structural, anatomical, or behavioral differences (e.g., Guasparri, 2022). Aristotle was among the first to depart from this fabric of generality in establishing a way of knowing based on observation and most importantly, dissection of specimens, in a process and using methods we now recognize as comparative morphology. We can trace rudimentary ideas of shared morphological similarity and the signatures revealed about organismal diversity to the *Historia Animalium* (Inquiry About Animals—see the discussion of Aristotle in Romero, 2012). Indeed, our current methods of observation and integrated analyses confirm the validity of about 550 to 600 species described by Aristotle. Alas, for Aristotle his taxonomy depicted the boundaries of an immutable, static world, steeped in teleological explanations, causality, and with a trajectory of a purpose in natural systems devoid of the rich history of evolution.

Form and function related a story of fundamental relationships among organisms, confirmed by empirical evidence and powerfully concordant theories of complexity as a hallmark of Darwinian evolution, genealogy, and the tree of life (Agosta and Brooks, 2020). Among many scientists, and possibly most prominently among parasitologists, a group that we know intimately, the traditional endpoint had been the name and the description of an organism, often unconnected to a place, a host, or more revealing ecological and historical circumstances. A name and a handful of specimens, divorced from context, is utilitarian but misses the most powerful point. Names in isolation can never provide rigorous natural history explanations and should not be confused or conflated with deeper insights about the biosphere. Thus, our formalized taxonomies of Latin binomials, emerging nearly 300 years ago, remain incomplete,

misleading, and nondimensional without a full appreciation of diversity, phylogenetic connectivity, and natural history. Much of this history and baggage in taxonomy persists today, and in many ways does not extend our science beyond the philosophical approaches of Aristotle over 2,000 years in the past.

Names, which form the basis for our taxonomies and nomenclature, must serve as the gateway or portal to holistic biodiversity information about history, evolution, ecology, and biogeography (geographic distribution) that is organized and accessible in a phylogenetic context (Brooks and Hoberg, 2000; Wheeler, 2010). The process of naming in a phylogenetic context allows entry to explicit hypotheses about evolution and history—this is curiosity with a purpose (Brooks and McLennan, 2002; Wheeler, 2004). Curiosity without purpose—the singular act of naming, building taxonomies and nomenclature, that remain without a context of natural history and phylogeny in a world under rapid perturbation—is increasingly a luxury.

Although names and phylogeny are the anchors for understanding diversity, a confounding factor is the apparent temporal asynchrony in the process of speciation and formation of species in space and time. Organismal asynchrony is particularly problematic in the realm of viruses and bacteria. Rapid rates of evolutionary change challenge our abilities to recognize the oscillations associated with species formation and subsequent disappearance on fine geographic and temporal scales before adequate study and evaluation is possible (see Souza et al., 2022). Highlighted is the operational challenge and difficulty in creating viral classifications and associated taxonomies that embody a nomenclature also connected to natural history.

Insights about the complex dynamics of emerging disease are fully dependent on the validity and authority of names for pathogens and hosts, and their identities, phylogenies, and natural histories. Named specimens and associated biodiversity informatics should provide an essential foundation for One Health, although such is currently lacking (Colella et al., 2021; see Cook et al., 2004; Coker et al., 2011; Gebreyes et al., 2014; and <https://www.cdc.gov/onehealth/index.html> for mainstream definitions of One Health).

As understanding about the nature of overlapping and synergistic crises for climate, biodiversity, and emerging infectious diseases has become increasingly focused (e.g., Brooks and Hoberg, 2013; Brooks et al., 2019; and references therein), so has explicit recognition of the connectivity between animal, plant, and human disease, facilitated by environmental opportunities. These interactions and outcomes led veterinary scientists and clinicians to embrace what is called One Health (Zinsstag,

2011; Cunningham et al., 2017) and more recently Planetary Health (Horton and Lo, 2015). Unfolding in the 1940s, One Health initially brought together a coalition of veterinarians, physicians, and a broader range of organismal biologists, with foundations in the Centers for Disease Control and the U.S. Public Health Service. Planetary Health is a complementary and more explicit approach that transcends pathogens to understand the connection between accelerating climate change, unprecedented environmental perturbation, and human health, with origins in the Rockefeller Foundation–*Lancet* Commission on Planetary Health in 2014 (Horton and Lo, 2015; Whitmee et al., 2015; Watts et al., 2018).

Common to these proposals has been the recognition that transboundary and interdisciplinary cooperation is needed, bringing ecology, biodiversity, environmental health, and medicine to the forefront in addressing increasingly complex challenges for humanity and the human landscape. In contrast to earlier independent and limited explorations that emphasize single organisms or regions, our understanding that rapidly changing environments from which viral, bacterial, fungal, arthropod, and helminth pathogens emerge demonstrates the urgency for new ways to coexist and live with our world (Brooks et al., 2019). The One Health and Planetary Health trajectories are positive steps, although they remain divorced from broader explorations of the biosphere and the global umbrella of environmental settings, history, and biodiversity that describes the extensive interacting assemblages of hosts, reservoir hosts, and pathogens in circulation (Hoberg, Boeger, Brooks, et al., 2022).

As an often-siloed assemblage of disciplines with loosely organized components, One Health has remained uncoordinated, response-based, and reactive in nature, usually with the goal of detection and identification of pathogens post-emergence (when it is essentially too late for prevention). Fundamentally, One Health pathways unfold as a continuation of business as usual, with limited connections to evolutionary biology and natural history (summarized in Brooks et al., 2019; Colella et al., 2021; Trivellone, Hoberg, et al., 2022). In this arena, authoritative names too often escape attention and consideration in the predominant approaches to zoonoses. In contrast, the potential of a proactive stance on emerging infectious disease (EID) is intimately linked to nomenclature in understanding the diversity and distribution of pathogens and hosts. Proactive foundations can be realized through the power of biological collections, which connect field biology to permanent archives and phylogenetic insights synthesized in cumulative, digital, and publicly available informatics resources. A potential and proactive trajectory for

One Health can be articulated under the evolutionary umbrella of the Stockholm paradigm (SP) and across the operational components of the DAMA protocol (Document, Assess, Monitor, Act) (Brooks et al., 2014, 2019; Colella et al., 2021; Agosta, 2022; Brooks, Boeger et al., 2022; Hoberg, Boeger, Molnár, et al., 2022; Trivellone, Hoberg, et al., 2022; and references therein).

Our current pathways for pathogen detection often disregard and hinder the identification and elucidation of the source(s) of essential information, as denoted by inadequacy and limited interoperability of data streams related to assessments of pathogen/host diversity in the viral realm (e.g., Plowright et al., 2019; Ruiz-Aravena et al., 2021). Discordance and disconnects highlight the need for improved communication and clear protocols, not only for the spatial and temporal dynamics of sampling regimes but most critically for development of biological archives and databasing of vast and integrated information streams. Protocols should encompass holistic and strategic/targeted sampling of hosts, specimens, and pathogens and expansion of informatics resources directly linked to specimens held in fully accessible museum repositories (e.g., Gardner, 1996; Gardner and Jiménez-Ruiz, 2009; Dunnum et al., 2017; Galbreath et al., 2019; Colella et al., 2021). Again, assumptions about pathogen and host identity are only assumptions in the absence of verifiable voucher specimens.

Ultimately, a primary goal is complete sharing and accessibility of diagnostically relevant data, including sequence-based, genomic, isotopic, behavioral, and morphological information with standardized metadata in public repositories (NASEM, 2020). As has been noted in the course of the SARS-CoV-2 pandemic:

*The impact of genome data (or any molecular data) is dependent on their quality, and (how) the reliability and accuracy of such data may influence the global community's ability to track the emergence and spread of variants in a timely manner. (Chen et al., 2022)*

In the latter situation, uniform accessibility by the international community to synoptic data sources for diagnostic sequences across the time frame of the current pandemic has remained limited. DNA sequencing—fast genotyping—may indeed represent the only manner of recognizing evolutionary changes in rapidly evolving lineages of microparasites such as bacteria and viruses. In a way, sequencing is the nomenclature of the moment. Sequences, like names, connect past and present, allowing recognition of spatial and temporal connectivity for pathogens in the future through phylogeny.



## No Specimen, No Name, No Information

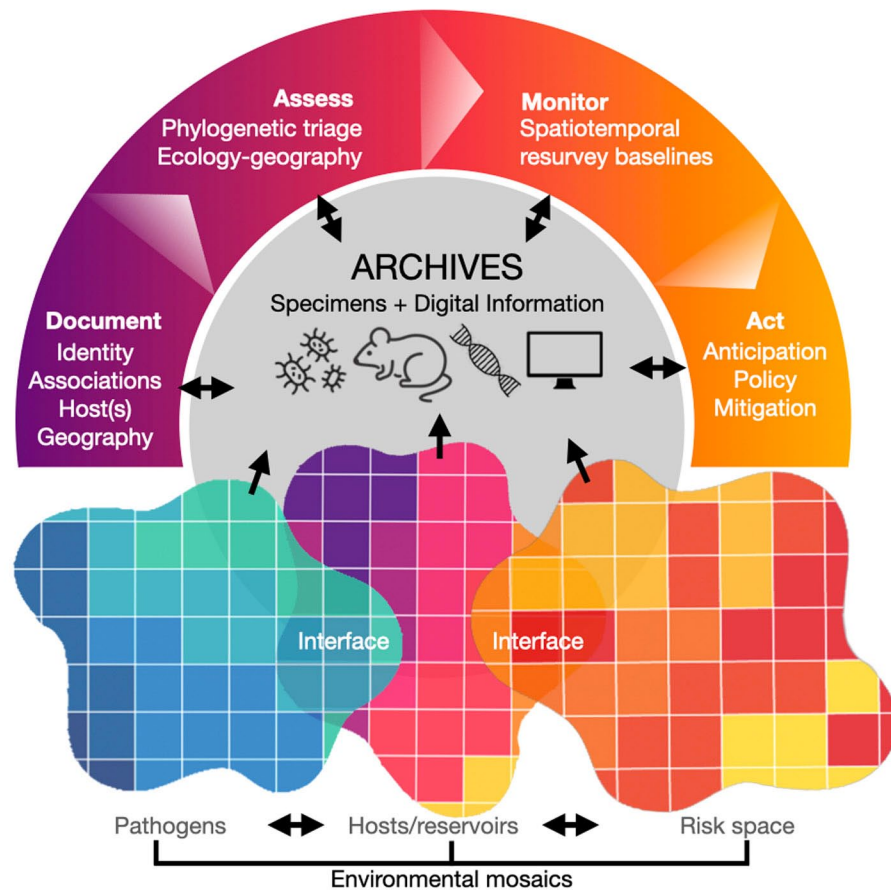
Names originate from specimens—the window on the world that is held in museum archives and biorepositories (e.g., Hoberg, 2002; Wheeler, 2010; Dunnum et al., 2017; Cook et al., 2020; Thompson et al., 2021; Naggs, 2022). Harkening back to Aristotle on the island of Lesbos, as scientists we explore the world, collecting specimens, continuing to poke and prod, using increasingly sophisticated toolkits from 3D morphology to isotopic chemistry and genomes in pursuit of insights about the assembly, distribution, interactions, and history of diversity. As for Aristotle, and no less in the current timeframe, everything begins with specimens.

In current systematic biology, this concept is solidified through permanent archives of whole organisms and associated tissues, genes, metadata, and information derived from specimen-based studies, which are fundamental to an integrated understanding of diversity. A prescient lesson from around 320 BCE about describing the biosphere highlights the importance of direct observation of a specimen in hand because in the absence of physical specimens all information cannot be confirmed or refuted and is immediately suspect (e.g., Hoberg and Soudachanh, 2020, 2021). Specimens validate names and collectively within their evolutionary context validate interpretation of complex data streams. There is an elemental trajectory through specimens to observation and information, from which synthesis and narrative emanates, contributing to emerging theories describing assembly and nature of the biosphere through space and time. There should always be a pathway from field-based specimens to permanent archives to shared biodiversity informatics and synthesis (Naggs, 2022). Increasingly, the global community of natural history museums is linking disparate data streams through development of accessible digital formats that integrate physical resources of specimens with deeper insights that bridge natural history, phylogeny, ecology, and biogeography in the realm of *cyber-taxonomy* (e.g., Wheeler, 2010; Cook et al., 2020; Colella et al., 2021; references therein).

Specimens and collections resources, despite the dimensions of some prominent international museums, are increasingly and habitually shuttled off to the dark corners of biology in many institutions (Naggs, 2022). Building specimen infrastructure, especially large series that provide extensive and intensive snapshots of the biosphere, has been the focus of a relatively few dedicated systematic and evolutionary biologists. More often, however, such series are never accumulated and preserved because specimens are often an afterthought in the day-to-day practice of ecology, conservation biology, and explorations of planetary biodiversity (Cook et al., 2016). Or, if specimens

are accumulated and explored, such may be passively discarded after assumed identification or application to a narrow question, despite the ever-evolving nature of new toolkits to reveal the dimensions of diversity (reviewed in Colella et al., 2020, 2021, references therein). Eventually, often as orphan personal research collections, in the wake of academic and professional turnover, specimen resources are separated from data and lost in the recesses of slide boxes, bottles, cryovials, and ultracold freezers. Specimen and information loss, either passive or as an active decision, is not new but a pervasive outcome in the continuing trend for inadequate resources and especially limited critical mass for taxonomists and natural history collections encompassing all taxa despite circumstances of increasing global urgency (e.g., Brooks and Hoberg, 2001; Wheeler, 2010; Cook et al., 2020; Naggs, 2022). Specimens seem to fall under the hubris of the *Dangerfield Principle*—often receiving little respect from a heterogeneous community of field biologists, practitioners, disease ecologists, and other scientists whose activities are directly dependent on the availability of permanent archives of specimens, authoritative names, and associated informatics. Specimens validate names, and names enable robust exploration and testing of hypotheses that validate our theories about assembly and nature of the biosphere through space and time. Ultimately a robust understanding of pathogens and disease can emerge from a rigorous adherence to data collection, feeding into well-supported infrastructure that describes the complex umbrella of global biodiversity (e.g., Brooks and Hoberg, 2013; Drabik and Gardner, 2019).

Documentation of the biosphere through specimens and their metadata deposited and linked in well-connected museums should not be an afterthought in the scientific process but instead a strategic imperative (Hoberg, 2002; McLean et al., 2016; Schindel and Cook, 2018; Miller et al., 2020; Gardner et al., 2021). Although opportunistic activities can provide glimpses of the biosphere, such approaches fail to build a robust, coordinated, and strategic view of spatial and temporal complexity. Limits of host and geographic ranges for pathogens, patterns of diversity, and disease are required to understand distribution and risk space for circulation and emergence (e.g., Audy, 1958). Documentation must be strategic and aim to account for elements of heterogeneity in diversity, with distinct and disparate rates of evolutionary change and vagility because for many viruses and bacteria diversification is considerably more rapid than weeks, months, or even the stretch of a human lifetime. Consequently, some taxa may necessarily require consideration of the time frames and time series that can maximize exploration of lineages, geographic distribution, evolution, and novel patterns of emergence (e.g.,



**Figure 1.** Conceptual framework illustrating the centrality of archival research collections to the DAMA protocol: Document, Assess, Monitor, Act. Collections must be representative of the changing mosaic of space, time, and environmental complexity across both pathogens and hosts.

Botero-Cañola et al., 2019); also see Boeger et al. (2022), Hoberg, Boeger, Brooks, et al. (2022), and Holmes (2022) for succinct summaries of the history of SARS CoV-2. Synoptic data streams that are publicly available can allow us to explore the relationship of pathogen reservoirs and environmental interfaces.

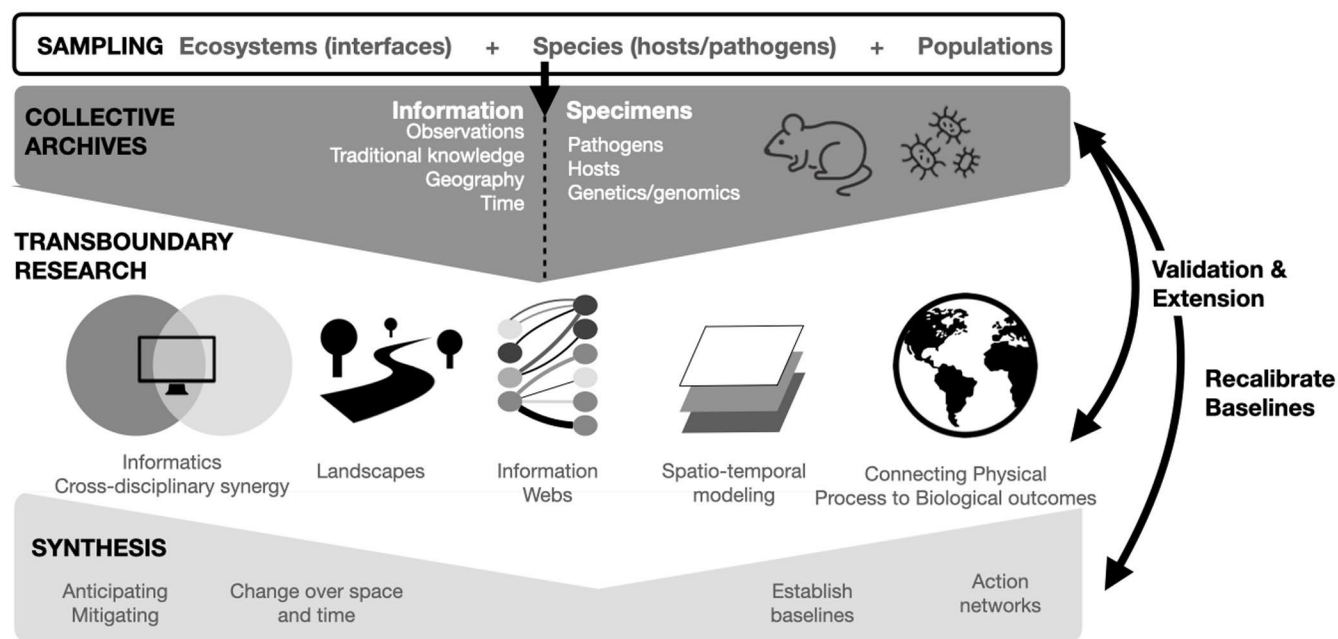
Complex data streams allow integration across space and time on a planet experiencing accelerating change, as exemplified by the proposal for the **DAMA protocol** (Brooks et al., 2014, 2019; Colella et al., 2021; Brooks, Boeger, et al., 2022; Brooks, Hoberg, et al., 2022; Hoberg, Boeger, Molnár, et al., 2022) (Figure 1). Where appropriate, geographically extensive and site-intensive, field-based inventories of communities of organisms, preserved as specimens and digitized information in natural history collections, should be at the core of **Documentation** (Hoberg, Boeger, Molnár, et al., 2022). Incorporated into **Assessment**, specimens with authoritative identification that are placed in a molecular phylogenetic context, are the first step in triage, which defines the extent of risk space (Hoberg, Boeger,

Molnár, et al., 2022). **Monitoring** through resampling and reassessment, paired with archival development of infrastructure for pathogens and hosts, contributes to temporal and spatial baselines, providing windows into identified environmental interfaces and the ever-expanding array of host reservoirs under environmental transformation (Botero-Canola et al., 2019; Hoberg, Boeger, Molnár, et al., 2022). The linked steps of assessment and monitoring provide real-time insights about the distribution of risk (and patterns of pathogen distribution relative to patterns of emergent disease), tracking ecological and evolutionary changes that influence risk space and the interface of opportunity and capacity (e.g., Zhao et al., 2022). Collectively these insights contribute directly into **Actionable** information for dissemination that allows us to anticipate and mitigate enzootic, epidemic, and pandemic emergence (see Brooks, Boeger, et al., 2022; Ortiz and Juarrero, 2022; Hoberg, Boeger, Molnár, et al., 2022). We are left to inquire: If specimens are fundamentally important, why are they so rarely preserved, tabulated in a database, and archived?

A cogent case study of this conundrum is seen in the current spotlight focused on viral species richness among mammals. Seeking to document, predict, and understand the limits of viral diversity and patterns of host and geographic circulation has become a foundation of pandemic biology—that is, efforts to identify direct links between viral pathogens and diseases emergent in humans (Grange et al., 2021; and references therein). Over the past 15 years biological field collections have explored assumed viral hot spots as defined by global geography (e.g., Jones et al., 2008). To be sure, these studies have dramatically broadened our knowledge of viral pathogens and have enabled biologists to refine estimates of total species richness for assemblages of viruses globally in such mammalian groups as chiropterans and rodents (Young and Olival, 2016; Olival et al., 2017; Mollentze and Streicker, 2020; Zhou et al., 2021; Carlson, Albery, et al., 2022). Critically, however, authoritative identifications of host species have been largely ignored, despite calls for broadening efforts to integrate surveys that link field collection and museum deposition, especially of bats (Gardner and Jiménez-Ruiz, 2009; Gardner and Whitaker, 2009). Globally, few host or pathogen specimens have actually been archived, and our current and future knowledge of their diversity and distributions

effectively has been lost to science and society. For example, nearly 75,000 mammalian specimens were handled or collected during the duration of the PREDICT program (e.g., in part summarized by Grange et al., 2021), but relatively few have been archived in museum collections, particularly from regions of the world with considerable gaps in knowledge of species richness for rodents, bats, and other groups. Absence of critical archival vouchers for chiropterans and other mammals remains as a common practice in the most recent evaluations of SARS-like viruses circulating among bats in Southeast Asia, the presumed region of origin for the current pandemic (Latinne et al., 2020; Zhou et al., 2021; Temmam et al., 2022). Indeed, over the past 2 years surprisingly few diagnostic sequences that document the origins and circulation of variants for SARS-CoV-2 have been archived in permanent repositories (Chen et al., 2022).

We can do better, although such a shift will require a substantial cultural transformation in fieldwork, biological research, public health, and specimen curation that emphasizes expanding infrastructure, personnel, and informatics resources, driving a new paradigm for integrative collections and archives (Dunnum et al., 2017; Schindel and Cook, 2018; Colella et al., 2020; Thompson et al., 2021) (Figure 2).



**Figure 2.** Archives of information and physical specimens can be accumulated overtime through collective deposition of samples with natural history museum archives. These data fuel transboundary research, including but not limited to: cross-disciplinary informatics, landscape level analyses, information webs, spatio-temporal modeling, and connecting physical processes to biological outcomes. Such research leads to major advances in our synthetic understanding of the biosphere, facilitating anticipation and mitigation of emerging pathogens and change through time, informed establishment and recalibration of baseline conditions, and action in the form of public and health policy and conservation. Importantly, the persistence of research archives is what allows for scientific validation and extension.



Discussions about the nature of biological (collections) repositories have been in development for more than two decades, with only minimal change in practices and the manner in which most institutions link natural history from fieldwork, to the laboratory where specimens are processed, analyzed, interpreted, and disseminated as vital, useful, accessible, and actionable information (e.g., Brooks and Hoberg, 2000; Hoberg, 2002; Wheeler, 2010; Brooks et al., 2014; Schindel and Cook, 2018; Cook et al., 2020; Gardner et al., 2021; Chen et al., 2022). Concurrently, during this period of increasing and overlapping global crises, some historically critical repositories, including the Natural History Museum, London, are poised to discard a deep legacy in biological diversity and systematics initially established more than 250 years ago derived from specimens deposited there from the early explorers in the 17th century (Naggs, 2022).

The urgency of an effective One Health under an evolving paradigm is not simply a question of the dynamics of humans, vertebrates, pathogens, and their links and associations to the animal world. Human well-being across the planet is no less an outcome of food and water security, reflecting the cascading environmental challenges posed by pathogens and diseases of food animals and crop plants in agriculture as a broader component of One Health and Planetary Health (e.g., Whitmee et al., 2015; Watts et al., 2018; Brooks et al., 2019; Benton et al., 2021; Wilcox et al., 2021; Brooks, Hoberg, et al., 2022; Trivellone, Hoberg, et al., 2022).

## The Nature of Specimens and the Borders of Information

Philosophically and operationally, typological thinking dominated practices to name and describe species for much of the past 200 years, and adherence to typology in part represented an absence of vision and imagination. Although a static view of biodiversity may have been acceptable a century ago, it is no longer tenable. Among taxonomists, the type was the *one exemplar* and name-holding specimen that served as the representative individual or embodiment of a particular species against which all others would be compared. A type seemed sufficiently emblematic of a species prior to the advent of evolutionary biology and an understanding of the limits for geographical, morphological, and most recently molecular variation. In parasitology, a traditionally host-centric view of parasite diversity and distribution served to further elevate the type. For example, conceptually knowing the host could be equated with knowing the parasites, a core mantra of the past century (e.g., Brooks et al., 2019). An expectation of

host specificity and association by descent (cospeciation) provided a convenient path, a simplified view of diversification and faunal assembly in which to contextualize diversity and limits on community change (e.g., Hoberg and Brooks, 2010; Brooks et al., 2015; Hoberg et al., 2015).

Fortunately, we are beginning to abandon this simplicity by replacing it with a nuanced picture of complexity as a more inclusive and overarching umbrella for global biodiversity—a story explored elsewhere under the SP (Hoberg and Brooks, 2015; Brooks et al., 2019; Agosta, 2022; Agosta and Brooks, 2020; Brooks, Boeger, et al., 2022). We now know that a name by itself, a type, and a mere handful of specimens of either pathogen or host(s) are not sufficient to resolve the critical issues related to zoonotic pathogens and environments that represent risk space for humanity, our domesticated animals, and our crops. Speaking of macroparasites and microparasites, museum collections are more often populated by types and type series (required by the International Code of Zoological Nomenclature; ICZN, 1999) and incomplete series of vouchers that reflect apparently novel host or geographic records. Vouchers are very rarely uniformly represented and archived from geographic or host surveys at any scale (consistent with Colella et al., 2020; Thompson et al., 2021). Published records linked to vouchers are uneven, seemingly like islands of enlightenment in a wide sea that limits key information and integration. Collections have historically served as gatekeepers, often siloed taxonomically and typically disinterested in archiving materials accumulated from survey and inventory. Further, there are no uniform requirements across a broad spectrum of journals (i.e., another set of gatekeepers) that specify or require deposition of vouchers for either pathogens or hosts (Schilthuizen et al., 2015).

Identification across many groups of pathogens (e.g., among macroparasites) has remained linked to host association under the idea that knowing the host provides fundamental insight into knowing parasite identity and to expectations emerging from assumptions about cospeciation and specificity (Nylin et al., 2018; Brooks et al., 2019). Identity linked to host taxonomy rather than parasite attributes, whether morphological or molecular, continues to codify a centuries-old, host-centric expectation of the distribution of parasite diversity that has been powerfully refuted (e.g., Agosta et al., 2010; Brooks et al., 2015, 2019; Nylin et al., 2018). Host-based identification of parasites, however, continues as a common theme in wildlife biology and veterinary medicine, and such identifications can and will remain unchallenged in the absence of archived specimens that can be examined and studied at a later time. Seldom is there room for argument about identity when no specimens serve as self-correcting records of diversity. For

example, consider nematodes (roundworms) among ungulates. In veterinary medicine, considerable parasite diversity, shared among wild and domestic ungulates, has been presumed as another manifestation of simplicity and often an assumed coevolutionary history (Hoberg et al., 2001; Hoberg and Zarlenga, 2016; and references therein). In contrast, interfaces between managed and wild ecosystems demonstrate a deep and increasingly complex picture of diversity (Hoberg, 2010). Temporal and spatial mosaics emerge as outcomes of dispersal and faunal mixing, an expectation under the SP (Brooks et al., 2019). In these ungulate communities, as an example of a larger generality, greater complexity is a consequence of parasite exchange over time. Faunal dynamics were driven by expansion, isolation, and multiple events of contact and host colonization in the Pliocene and Pleistocene, with secondary influences of regional domestication of ungulates in the Holocene and subsequent anthropogenic dissemination, tracking European conquests after the 1500s. Only from the context of specimens archived in biological collections, and through recognition of colonization processes in faunal assembly, can this convoluted historical tapestry, extending across Earth history, be disentangled (Hoberg and Brooks, 2008; Zhang et al., 2022).

To some extent, how taxonomists and a community of parasitologists in the broadest sense name species continues to represent fundamental assumptions about host associations. These assumptions are consistent with a history of one host (or one host group)–one parasite that was codified in the 1920s and is reluctantly being discarded among recent practitioners. For some, taxonomy established for a previously unrecognized species linked to a host is the convenience of conferring a name on a pathogen that leaves it easily identifiable. In the end, however, it does not reveal insights into history, ecology, or evolution. Notably, this isolated effort can be further confounded by the point that most species descriptions in parasitology remain the sole report of occurrence, and these isolated reports tend to bias ideas (and expectations) about host range (e.g., Carlson et al., 2020). Assumptions are equivocal in the absence of specimens, archives, and verifiable information. There is a *danger of convenience* when a worldview is not fully grounded by empirical data that can be verified and extended. It is hubris to think that something new cannot be learned from a specimen already examined. Convenience constrains broad-based thinking and misleads when there is reliance on suppositions about the nature and limits of diversity that are in error both conceptually and empirically (Brooks and McLennan, 2002; Hoberg and Brooks, 2015; Hoberg et al., 2015; Brooks et al., 2019).

In parasitology and entomology, and especially relative to macroparasites, comparative morphology must remain a gateway to exploring critical limits of diversity within an integrated framework that is in synergy with molecular data. An increasing shift, however, has been to diminish the essential insights derived from structural comparisons toward practices and assumptions that rely on molecular data as the sole or proper source on which to base species definitions and descriptions of faunal diversity. Another component of convenience is apparent in that over time cumulative capacities for comparative analyses are neither developed nor transferred to a new generation of scientists (e.g., Brooks and Hoberg, 2001; Poulin and Presswell, 2022). If we continue on this track, our future will then become an artifact of increasingly superficial taxonomy established in the past and extending into the present (e.g., Hoberg and Soudachanh, 2020). A parallel legacy will be information resources that are increasingly derived from non-invasive or nondestructive sampling that will leave us without permanent representation in specimen-based archives as vouchers, effectively limiting any possibility of replication and extension of the science (Colella et al., 2020; Rohwer et al., 2022). Further, apparent trends in large-scale ecological programs, such as the National Environmental Observatory Network (NEON) and the Circumpolar Biodiversity Monitoring Program (CBMP), away from true biological inventories, specimens, and archives with an expanding focus on noninvasive, observational data, including mark-recapture, do not effectively provide synoptic, large-scale snapshots that contribute to baselines of the biosphere in change (e.g., Hoberg et al., 2013; Cook et al., 2013, 2016, 2017; Christensen et al., 2021). Such programs, in the absence of strategic and focused field-based biological collections and specimens, will have a detrimental impact on capacities to identify assemblages of pathogens and hosts in transition.

## Archives and Natural History Collections—Truth in the Biosphere?

Operationally, how do we address pathogens and diseases in a world under dynamic transition? How would we track change in the biosphere if not for the insights that specimens can bring to the table with their names that we use as a shortcut to identity? Specimens and archives are the foundations for biological baselines in time and space against which change and transitions can be recognized and measured (Box 1, diversity of *Hantaviridae-Orthohantavirus*). When a valid taxonomy is lacking, the consequences are real. Consider the fact that even now in modern medicine, there is often less concern about the actual identity

**Box 1*****Hantaviridae-Orthohantavirus—the Classical Paradigm for Archives***

Orthohantaviruses (hantaviruses) are agents of disease among people in Eurasia (hemorrhagic fever with renal syndrome, HFRS) and the Americas (hantavirus pulmonary syndrome, HPS). The history of discovery, extending over much of the past half century tells a story about evolving perceptions and hidden diversity. Original misconceptions about host species and ranges may reflect conventional wisdom, in part established by the initial discovery and isolation of this group of viruses among rodents (e.g., *Apodemus agrarius*) from the Hantan River, Korea, in 1978 (Lee et al., 1978). This virus caused HFRS and was recognized in the 1950s in soldiers serving in the Korean War. There is, however, a history for recognition that extends considerably deeper in time. Further, prominent emergence of the *Sin Nombre orthohantavirus* from the Four Corners region of western North America was linked to infections originating in the deer mouse (then identified as *Peromyscus maniculatus*) and seemed to reinforce a history of association with rodents (Yates et al., 2002). Although there were early indications that these viruses may occur in other mammals (Song, Baek, et al., 2007; Song, Kang, et al., 2007), the idea that hantas were limited to only rodent hosts, and locked in an apparent co-evolutionary history with these mammals, appears to have constrained a broader search for diversity until the past few decades. The revelation that hantas were not solely found among rodents opened the floodgates for an expanding evolutionary picture (now including more than 139 distinct strains) that encompass viruses in chiropterans (bats) and eulipotyphlans (shrews and moles), in addition to a growing assemblage of rodents (Jonsson et al., 2010; Yanagihara et al., 2015; Liphardt et al., 2019; Arai and Yanagihara, 2020). Many of these discoveries were based upon mining frozen archives of rodent specimens collected previously for other reasons. Recognition of extensive diversity served to dispel the myth of histories linked to cospeciation for these viruses, with an extensive signature for bouts of host colonization into early mammalian evolution. For hantaviruses, initial perceptions about host range among rodents and the actual reality across mammalian diversity have served to uncover a potential minefield for emergent pathogens, emphasizing the crossroads for both opportunity and capacity. Not all of the news is good as we seek to unravel the global distribution of potential pathogens. Again, we run headlong into complications imposed by the absence of archives. Critical host data for more than two thirds of the currently recognized hantavirus strains are ambiguous and compromised because associated specimens and data are not held in permanent museum repositories, severely limiting our ability to confirm host identity or even extend previous work.

In contrast, the story of *Sin Nombre* tells us again about the interface for archives and urgent biodiversity discovery, and the integration of biorepositories, names, and critical information. The multiuse nature of biological collections forms the backdrop for a biological detective story. A disease was lurking among the undulating landscapes of the Four Corners, a stunningly beautiful desert landscape that links New Mexico, Arizona, Colorado, and Utah. It wasn't there every year, it wasn't known to the disease ecologists in any coherent way, but it resided in the extended memories and oral history of Navajo and other Indigenous peoples of the region. In the spring of 1993, an outbreak of a severe respiratory illness killed 10 people in an eight-week period, eventually leading to a 70 percent mortality rate as the disease progressed. The pathogen turned out to be a previously unknown virus in the hanta group, pathogens hosted by rodents in many regions of the world that often occur as serious zoonoses. The virus was eventually called *Sin Nombre* virus (Spanish for "without a name," abbreviated SNV). Field collections in the Four Corners ensued, and the host involved was identified as the ubiquitous *Peromyscus maniculatus*, the nondescript North American deer mouse. But where had the virus come from? Had it been introduced? Hantavirus was at that time rarely known in the Western Hemisphere. Museum collections of rodent specimens and tissues, along with human specimens from undiagnosed disease outbreaks, demonstrated that the virus had been present for decades and likely centuries or millennia. It was literally the stuff of legends, a mysterious disease that had persisted in the oral histories of Indigenous people. Archival frozen tissues revealed the history of the virus and were initially the window through which the question of origins could be examined. In the absence of collections, our current knowledge of hanta in the Americas would have been delayed for a considerable period of time. Nor do we always understand the biotic and abiotic factors that catalyze the shift from quiescence to disease. Sometimes it results from changes in ecological conditions, as turned out to be the case with *Sin Nombre*. The El Niño Southern Oscillation, a shift in the ocean and atmosphere that disrupts the Northern Hemisphere and beyond, produces unusually heavy rains that lead to an explosion of vegetative growth, seed production in pinyon and juniper woodlands, and increased arthropod biomass. Many animals, including deer mice, take advantage of this bounty and convert available resources into rodent offspring. Although not directly transferred to young, the increased viral prevalence for *Sin Nombre* comes from high densities of rodents in contact and horizontal passage of the pathogen. Expanding rodent populations explore new areas, including the interfaces of human habitations, and contact between humans and hanta is achieved (Yates et al., 2002).

of an organism that is causing a malady than the emergent disease syndrome (e.g., Robles et al., 2018; Kobayashi et al., 2019; Reuben et al., 2020). We identify symptoms and treat them, assuming the presumed pathogen (probably a virus) is unimportant, seldom seen (a rare event), or unlikely to be new. That a disease will disappear as quickly as it emerged is yet another misconception about the nature of hosts, pathogens, and their intertwined geographic distributions. The notion of disappearing pathogens was effectively dispelled nearly 60 years ago by a British disease ecologist named J.R. Audy who was working in Kuala Lumpur, Malaysia, where he noted the complicated spatial and temporal mosaics that described the shifting occurrences of pathogens and disease (Audy, 1958). We often forge ahead in the absence of a name, which demonstrates the tenuous link between academic taxonomies and clinical taxonomic practices.

Initial emergence of SARS-CoV-2, after all, was reported as a series of unspecified pneumonias among a small number of patients in central China. The short but intense global history of COVID-19 emphasizes that a common set of symptoms can be produced by more than one pathogen (consider seasonal influenzas and flu, varying sources of pneumonias), and no one can immediately recognize the difference or the etiological agent for a period of time without technological aid. We thus practice deferred diagnostics, and in the absence of definitive information, we make guarded assumptions about disease causation, and thus we remain mired in a response-based approach to EID (e.g., Brooks et al., 2014, 2019; Hoberg and Brooks, 2015; Boeger et al., 2022; Trivellone, Hoberg, et al., 2022).

We pass daily through a world of orphan viruses, and among these how many unknown viral pathogens are potentially emergent (e.g., Carlson, Albery, et al., 2022)? Identifying pathogens and the events associated with circulation, proliferation, and emergence is a considerable challenge, given the interaction of expansion waves and population sizes (of hosts and pathogens) on the margins of rapidly changing distributions. This is the dynamic described across pathogen diversity from the viral pandemic of SARS-CoV-2 to epidemics and recurrent outbreaks of Ebola or Zika to obscure lungworms and vector-borne nematodes among Arctic ungulates (e.g., Laaksonen et al., 2015; Kafle et al., 2020; Hoberg, Boeger, Brooks, et al., 2022; Regala-Nava et al., 2022). Because we can't easily observe the initial stages of expansion or emergence, a new term—"silent spillover"—has been proposed (Temmam et al., 2019). Pathogen expansion is "silent" only because for a time it may be hidden. Silent spillover is a misnomer because we are seldom seriously looking (i.e., with rigorous surveys), and we apply inexpensive and cursory pathways

to documentation and descriptions of biodiversity that are lacking in historical context; thus, the term is completely anthropomorphic. Again, we defer to Audy (1958), who recognized that the distribution of a pathogen is far greater than the distribution of disease caused by that pathogen, described the wobbling oscillations and seemingly ephemeral mosaics or islands of pathogens and disease, and made the point that pathogens never really disappear from landscapes and regions.

Names are assumed to be the truth, to be authoritative, and to reflect the reality of situations and circumstances. The foundations and implications of taxonomy apply equally to hosts and to pathogens, and we are continually challenged to get it right because there are distinct consequences, as we have seen, for getting it wrong (Box 2, diversity of *Borrelia*). Often, we discover secondarily, as archival biological collections are more deeply probed, that the host name attached to a pathogen is not the right one. For example, among the host assemblages for hantaviruses, critical taxonomy among genera and species of rodents has been in flux, reflecting a reassessment of the identities of some pathogen reservoirs following their original descriptions (Thompson et al., 2021). Among pygmy rice rats (genus *Oligoryzomys*), these insights demonstrated the potential for restricted geographic distributions for many reservoir hosts of hantaviruses (e.g., González-Iltig et al., 2014; Weksler et al., 2017). Vouchered mammal specimens that turned out to be actual host specimens have led to an increasingly refined view of host associations for numerous hantaviruses of significance in public health (Firth et al., 2012). In all situations, and not simply limited to hantaviruses, taxonomy matters, and apparent errors in identification are a direct impediment to defining host range, potential and realized patterns of circulation, and the elusive but critical definition of risk space. What is the outcome in the absence of biodiversity archives? Our understanding is immediately suspect, we likely will mischaracterize cryptic diversity, and our appreciation of the biosphere suffers in that we are unable to define putative species associations that are often hiding in plain sight.

We further confound descriptions of diversity by the choices we make in naming species, especially the names we propose for pathogens. Perceptions are critical and often become dogma. Thus, as an explanatory identifier, names are often proposed based on a disease syndrome in a particular host and become a manifestation of ideas about limited host range detached from natural history; names in the end are a shorthand identifier (Box 3, diversity of phytoplasmas). Names are also proposed for geography, the idea that the type locality (like the type host) has special biological meaning. Virology has a long tradition of



**Box 2****A Story of Burgeoning Diversity for *Borrelia* spp.**

Lyme disease is among the most significant vector-borne pathogens in the Northern Hemisphere and may have a broader occurrence in South America and Africa than previously understood—no one knows with certainty (Robles et al., 2018). The story of the causative agent of Lyme disease or Lyme borreliosis highlights the significance of accurate and complete taxonomy, which contributes to robust diagnostics (Kobayashi et al., 2019). Over time, our baseline information expands, showing the cumulative process of science in discovery of diversity and in defining pathogen distribution and outcomes of infection. Original concepts established ixodid (hard-bodied) ticks in transmission of a single spirochaete bacterium, *Borrelia burgdorferi*, occurring in an assemblage of mammals and sometimes birds (e.g., Ostfeld and Keesing, 2000). Human infections arose through opportunity at environmental and management interfaces, where ticks, reservoir hosts, and pathogens were in circulation. A single pathogen species, however, seemed incompatible with a growing picture of the variable outcomes for disease depending often on geography in North America, Europe, or South America (e.g., Robles et al., 2018). Diagnostics suitable in the Northern Hemisphere were often confusing or inconclusive beyond this geographic arena. Lyme disease was becoming a mystery. Names are important, underscored by the recent discovery that Lyme disease is actually caused by more than one species of bacteria, or a species complex, often with varying disease presentations (Stone et al., 2017). In excess of 21 genotypic species are now identified in the genus *Borrelia*—or a cluster of pathogens and diseases globally (Stone et al., 2017). Previously unrecognized taxonomic diversity, under a single name, has likely been responsible for considerable confusion attendant upon diagnosing, misdiagnosing, and treating Lyme disease from landscapes to regions and to continents where explanations linked to etiology for a single pathogen are misleading (e.g., Granter et al., 2016; Álvarez-Hernández et al., 2017; Kobayashi et al., 2019). Coinfections with a broader assemblage of tick-borne pathogens may further confuse diagnosis and treatment (e.g., *Anaplasma phagocytophilum*, *Babesia* spp., *Ehrlichia* spp., *Rickettsia* spp.), reflecting variation among ixodid species and geography. Differential diagnosis additionally is challenged by the occurrence of a wider range of pathogens that do not have tick-borne etiology (e.g., dengue, chikungunya, Zika, and leptospirosis). Consequently, misdiagnoses are common—and as Kobayashi et al. (2019) have noted—“. . . that regardless of test results, Lyme disease is the diagnosis used to explain the mostly subjective symptoms. Patients and clinicians may be influenced by alternative, non-evidence-based medical practices, or could be confused by non-validated laboratory test results or interpretations.” Strategic field-collections and development of archives encompassing pathogens, mammalian reservoir hosts, and arthropod vectors, along with historical clinical information are required to explore the complex dynamics of circulation for multiple pathogens such as *Borrelia* spp. under a DAMA protocol (Brooks et al., 2014). As a generality, accelerating climate change and environmental disruption are anticipated to directly influence distribution of pathogens and disease (e.g., Brooks and Hoberg, 2007; Ostfeld and Brunner, 2015).

naming viruses that reflect focal localities: consider Ebola (for the Ebola River in 1976), Marburg (for a town in Hesse, Germany, in 1967), and Prospect Hill *Orthohantavirus* (for Prospect Hill, Maryland, in the 1980s), among many others. Unfortunately, the geographic name attached to a first discovery can take on a particular caché that some consider an indicator of limits on (or a limited) spatial distribution, although in all cases the distributions are considerably broader. In conjunction with a geographic source, pathogens may receive names that denote the disease and the regional locality—for example, Bolivian hemorrhagic fever virus (BHFV) (also known as Machupo virus after the river where it was first identified), Middle East respiratory syndrome virus (MERSV), or severe acute respiratory syndrome virus (SARSV)—and especially the disease as it is

manifested in the originally recognized host, which is often not the reservoir responsible for maintenance and circulation. Some are denoted to describe special aspects of disease, such as chikungunya virus (CHIKV), found in Tanzania in 1952 and named from a local dialect term for “to become contorted.” Lastly, we name parasites based on our assumptions about host association. Much of this taxonomy reflects responses in human hosts for zoonotic viruses for which emergence is often initially recognized. Often it is only later that natural host assemblages, including various arthropods and vertebrate reservoirs for arboviruses, which drive colonization events are documented. Our choices for naming can be misleading in the absence of authoritative information, and there are no authoritative names or informatics for either hosts or pathogens in the absence of

**Box 3****Uncovering the Overlooked Extant Diversity of Phytoplasmas**

Phytoplasmas are a diverse group of vector-borne obligate intracellular parasitic bacteria (phylum *Mycoplasmata*, class *Mollicutes*) associated with vascular plants and phloem-feeding hemipteran insects. Ecologically these represent a poorly known but critically important group for food security and environmental integrity. Since their discovery and characterization (Doi et al., 1967), they have been shown to be associated with severe diseases causing major economic losses in cultivated crops and other plants (Bertaccini et al., 2014; Brooks, Hoberg, et al., 2022). Still phytoplasmas remain among the least known of the *Mollicutes* bacteria. Prior research on phytoplasmas has mainly focused on their role as plant pathogens, aimed toward managing phytoplasma-caused diseases in agro-ecosystems. Previously known strains of phytoplasma were mostly discovered by screening economically important plants exhibiting disease symptoms. Phytoplasma infections, particularly in noncultivated native plants, are often asymptomatic (Zwolińska et al., 2019) and, therefore, may go undetected by plant pathologists surveying for plant diseases. Consequently, phytoplasmas have been largely named based on the main symptomatic spectrum exhibited by infected plants or based on the host itself. This has reinforced the misconception that specific groups or subgroups of phytoplasmas are restricted to particular host species (host repertoire) and thus occupy a limited geographic area or habitat (apparent host specialization). As recently summarized in a comprehensive database (Trivellone, 2019), phytoplasma-host data are limited by this shortsighted focus on cultivated plants and agro-ecosystems which introduced bias into preliminary network analyses and highlights shortcomings and gaps in knowledge of pathogen biodiversity (Trivellone and Flores, 2019). As vector-borne pathogens of plants, phytoplasmas evolved a fine-tuned intimate relationship with hosts and insect vectors on which they rely for survival and dispersal throughout the environment. Unfortunately, the vectors of most phytoplasmas remain unknown and the known vectors have been studied primarily from the perspective of plant pathology and epidemiology. Specimens of potential vectors are usually analyzed in pooled samples using destructive DNA extraction methods; that is, specimens are homogenized, and none are retained to serve as vouchers that demonstrate the insects were correctly identified. This methodology also makes it impossible to track the association between the pathogen strain and the individual insect (particularly if more than one strain is present in the pool). Recent research has shown that phytoplasmas have been evolving together with their hosts for more than 300 million years (Cao et al., 2020), manifesting a complex history of diversification. Notably, associations between phytoplasmas and their native hosts may be older than those documented in agro-ecosystems (Trivellone and Dietrich, 2021), and recent screening of insect specimens from a museum collection/biorepository has already begun to document new phytoplasma strains and new associations with potential vectors in natural areas worldwide (Trivellone et al., 2021; Wei et al., 2021; Trivellone, Cao, et al., 2022). Moreover, detailed digitized data on collecting events associated with specimens in the biorepository open further opportunities to study temporal series. The phytoplasma-hemipteran system is a critical exemplar of the continuing necessity to build collections infrastructure to establish a global view of dynamic diversity under the umbrella of the Stockholm paradigm.

archival specimens maintained in well-organized museum collections and databases, such as the Museum of Southwestern Biology (MSB) and the Harold W. Manter Laboratory of Parasitology (HWML) (Drabik and Gardner, 2019).

Viral taxonomies pose particular challenges and to a degree have remained outside of the bounds of conventions for multicellular diversity. Calisher and Yates (1999) proposed naming hantaviruses with a binomial nomenclature following universal taxonomic norms and based on the species name of their primary host (e.g., *Hantavirus maniculatus* for Sin Nombre virus). A methodology was intended to more closely tie a virus to its reservoir species, recognizing the essential nature of the proper association of a pathogen and its host. In response, and we concur, Bennett et al. (1999) agreed with the need for tying host to

pathogen but suggested the issues of misidentified host species and dynamic mammalian taxonomy (as outlined earlier) were hindrances to the success of this naming format. More recently, the International Committee on Taxonomy of Viruses Executive Committee (2020) proposed a new system to establish rank and classification with the following justifications:

*The codified availability of a greater number of ranks in a formal virus classification that emulates a Linnaean framework may also facilitate the comparison, and possibly improve the compatibility of virus taxonomy with the taxonomies of cellular organisms. Although the switching of hosts by viruses may be a complicating factor, . . .*

*We expect that the described changes to the hierarchical rank structure will create a new impetus for the exploration of virus macroevolution and a framework for its application to taxonomy. The changes will also stimulate research on the defining characteristics of monophyletic virus lineages and the recognition of historical events that played a decisive role in their origins and evolution.*

## Do You Know What You Have Named?

Correct names are the lingua franca, and these are derived from deep, fundamental assemblages of specimens and information held in permanent archives. Correct and complete names, when connected to phylogeny, are the linkage to essential context in the biosphere. Phylogeny and a phylogenetic diagnosis (what an organism is in space and time, defined within an array of unique and shared characteristics and relationships to other organisms) are fundamental to establishing the evolutionary, ecological, and biogeographic tapestry of life. From that tapestry we can identify the interactions within the SP (Hoberg and Brooks, 2008, 2015; Araujo et al., 2015; Brooks et al., 2019; Brooks, Boeger, et al., 2022; Hoberg, Boeger, Molnár, et al., 2022) and the nature of ecological fitting in sloppy fitness space (and phylogenetic conservatism), oscillation, taxon pulses (across hosts and geography), and coevolutionary mosaics that are the essence of a predictive and anticipatory framework for emergent pathogens central to the proposal for DAMA (Brooks et al., 2014; Colella et al., 2021; Agosta, 2022; Boeger et al., 2022; Brooks, Hoberg, et al., 2022; Trivellone, Hoberg, et al., 2022). Field-collected specimens accumulated across extensive geography, tempered in the strategic context of targeted interfaces that interconnect wildland habitats, peri-urban, and urban settings, and agro-landscapes representing assemblages of recognized and potential reservoirs are the core of DAMA (Figure 1). Archives of specimens lead to archives of information, and collections become fundamental resources for biodiversity informatics (Hoberg, 2002) under the umbrella of the *holistic specimen* and standardized methodologies (e.g., Frey et al., 1992; Cook et al., 2016, 2020; Galbreath et al., 2019; Phillips et al., 2020).

How and what we name is critical. The truth of a name, again, resides in that essential connection to specimens, evolution, ecology, and natural history. An unsubstantiated name is not good enough in our descriptions of diversity—when there is no justification provided from vouchers or specimens in published surveys, and often manifested in aspects of genomic and molecular prospecting, evaluation,

and analysis. Names are assumed to be the truth. Misidentification is not only an error but can establish a fallacy that can be further perpetuated by convenience (lack of archival specimens) in a deep global literature about the distribution and history of diversity (e.g., Hoberg and Soudachanh, 2020; Hoberg et al., 2009; Bush et al., 2021). Thus, how we use taxonomy can be misleading if it is no longer possible to revisit specimens and validate their identification or to explore and probe with new technologies and methods that dissect the world at increasingly fine scales. Misidentification is like a Gordian knot that can never be resolved. Misrepresentation, on the other hand, is scientific fraud of the highest order. Our stories always start with specimens and handwritten field catalogs. Data obtained in the field, with associated host and parasite data, then enter a convoluted path through various museums and archives, settling questions of science, arriving at names and a nomenclature that should be connected to phylogeny and evolution. How else can we come to agreement about how the biosphere is structured through space and time and especially related to the obscure and hidden minefield that is global pathogen circulation?

Proactive approaches to emergent pathogens and diseases are derived from an understanding of diversity (phylogenetic triage and spatial/temporal distribution) and capacity on the part of micro- and macro-parasites to use historically (evolutionarily) conserved host-based resources (Agosta et al., 2010; Brooks et al., 2019). These fundamental cornerstones provide the ability to anticipate colonization and emergence across changing environmental interfaces and are critically linked to actions (behaviors) that serve to break the links or pathways for opportunity. The SP, its operational extension in DAMA, and broadened development of archival resources for specimens and information can transform our understanding and approach to pathogens (Brooks et al., 2019; Colella et al., 2021; Hoberg, Boeger, Brooks, et al., 2022). Specimen-based trajectories are vital in developing, facilitating, and protecting access to cumulative information representing the baselines for recognizing changing environmental interfaces in the biosphere from natural to managed and agricultural systems and across landscape to regional and global scales (Figure 2). A proactive capacity unfolds, from natural to managed and agricultural systems, that is fundamental to both animal and human health and to food security (Brooks, Hoberg, et al., 2022; Trivellone, Hoberg, et al., 2022).

Continuing discussions call for program development of national and international scope to address the ecological and anthropogenic causation and increasing frequency of emergent diseases (e.g., Suzán et al. 2015; Brooks et al., 2019; Daszak et al., 2020; Dobson et al.,

2020; Gibb et al., 2020; Alimi et al., 2021; Keesing and Ostfeld, 2021; Brooks, Hoberg, et al., 2022; Carlson, Boyce, et al., 2022; Reaser et al., 2022). Yet, there remains a fundamental disconnect relative to those programs that advocate new directions for exploring pathogens and developing informatics resources but which have no apparent interdependence with permanent archival resources (Up- ham et al., 2021). Concurrently, intensive synthesis about the nature of specimens, archives, and digitized informatics about the biosphere or specifically about pathogens and hosts are seldom incorporated programmatically into disease ecology from landscape to regional scales (e.g., Cook et al., 2020; Colella et al., 2021; Hoberg, Boeger, Brooks, et al., 2022). Perhaps this disconnect also reflects an outcome of erroneous but prevailing expectations for the rarity and unpredictability of emerging pathogens in the global arena. Again, this situation emphasizes and calls for substantive cultural transformation in a dispersed but digitally connected community.

## Conclusions

A cultural and conceptual transformation is essential, one that recognizes the necessity of placing pathogens in an environmental, evolutionary, and ecological context by incorporating specimens and associated informatics into the foundation for actionable information. Specimens are naturally the nexus of collaborative networks needed to reveal the connectivity and complexity that embodies the biosphere (e.g., Hoberg, 2002; Colella et al., 2021) (Figures 1 and 2). Such an approach is consistent with the boundaries of the SP and its operational protocols under DAMA (Brooks et al., 2014; 2019; Boeger et al., 2022; Hoberg, Boeger, Brooks, et al., 2022). There is an exigency that extends beyond typical research cycles of 3 to 5 years in a world under rapid change and disruption (Colella et al., 2020; Brooks, Hoberg, et al., 2022; Trivellone, Hoberg, et al., 2022). Research groups to some extent have focused on pathogens or free-living assemblages of organisms, including plants and animals, but seldom both and seldom concurrently and almost always in narrow time frames defined by the finite cycles of grants. Business as usual in this arena perpetuates a disconnected and discordant landscape of untestable empirical observations and ideas. The possibility of and potential for the holistic specimen, deep synoptic repositories, integrated phylogenetics, and digitized standardized informatics resources linked to natural history are so critically essential yet have rarely been achieved (Brooks and Hoberg, 2000; Wheeler, 2010; Cook et al., 2013, 2017, 2020; Hoberg et al., 2013; Dunnum et al., 2017; Galbreath et al., 2019).

Historically, natural history repositories and archives have served us well in leading characterization of the biosphere and the interrelationships of natural, agricultural, managed, and urban systems. However, few broadly integrated collections drive comprehensive exploration of host-pathogen-disease dynamics. One primary exemplar is the Museum of Southwestern Biology (University of New Mexico, Albuquerque) with decades of sustained development of collections that integrate parasites, pathogens, and potential and actual reservoir hosts (e.g., Yates et al., 2002; Gardner and Jiménez-Ruiz, 2009; Cook et al., 2017). Even among pathogens and scientists we remain strongly siloed, and the generality of lessons revealed among viruses, other microparasites, and macroparasites are considered in isolation or in an organismal vacuum defined by taxonomy and assumed specialization. Notably, a substantial conceptual gulf continues to exist between the worlds of animal and plant pathogens and their respective vectors (e.g., Nylin et al., 2018). Collections are also limited in how they contribute or what they will receive. Programs and curators generally lack a coordinated global vision when a political arena determines infrastructure associated with national strategic plans and especially continuity and predictability of funds, personnel, and essential physical facilities (e.g., Naggs, 2022). As a consequence, curators too often may have to discourage deposition of large series of specimens from geographically extensive and site-intensive surveys that are central to understanding pathogen-host dynamics.

Our current reality is that historically, natural history collections were not designed to substantially contribute to a broader understanding of pathogen-host and disease dynamics; such was not their original purpose. In the absence of robust and additional support, current freestanding natural history collections may be to a degree ill-suited and poorly positioned to be able to accomplish what is necessary in the arena of EID. Not unlike the blind men and the elephant, our current infrastructure remains strongly partitioned. Whereas each taxonomic component has the potential for important contributions, each is not sufficient in isolation to constructively contribute to synoptic insights about pathogen distribution and emergence nor to policy actions linked to mitigation or prediction. Critically, this situation requires visionary people, additional resources, and better integration to effectively contribute to societal needs (NASEM, 2020). Appropriately, existing resources can be co-opted, repurposed, and consolidated to vastly improve descriptions of historical diversity over ecological timeframes and to forecast future conditions. As such these serve in a retrospective capacity, including pathogen discovery (e.g., Box 1, *Orthohantavirus* diversity, and Box 3, phytoplasmata diversity), but do not always contribute in



substantial and comparative ways to the development of baselines in the context of resurvey to reveal the trajectories of environmental change. Retrospective studies based on a literature in the absence of archives have particular limitations because of the potential for incorrect taxonomy (when voucher specimens are divorced from taxonomy), lack of comparability in methods and the scope of spatial and temporal sampling (e.g., Carlson, Boyce, et al., 2022). Insights are often limited to what we know (an array of known pathogens), not what we need to know nor what is unknown in circumstances of fluid interfaces and changing environments (e.g., Zhao et al., 2022). As a community we are continually surprised when the orientation of our current resources serves to perpetuate a largely response-based stance relative to EID.

A holistic framework for the “extended specimen” and outcomes for comprehensive surveys of pathogen-host associations has been previously articulated (e.g., Gardner and Jiménez-Ruiz, 2009; Cook et al., 2020). Conceptually, such a framework must be expanded to a proposition and then transformation to *next-generation natural history collections*, one that encompasses specimens, informatics archives, and digitized resources with broad accessibility and interoperability (Schindel and Cook, 2018). Collections can meet their potential as networked and integrated centers for pathogen-host diversity and biology, phylogenetics, ecology, and biogeography, which coordinate explorations of the nature of EIDs in an arena of accelerating environmental change. Understanding pathogens is essentially one of revealing the complexity and interconnections of planetary biodiversity. Holistic specimen collections would serve as validated clearinghouses for acquisition, interpretation, translation, and dissemination of informatics resources. Not simply an issue of wildland-managed interfaces, conservation, and species extinctions, the broader challenges to food security, domestic food resources, and agriculture must be accommodated within a comprehensive operational landscape for circulation of EID (e.g., Trivellone and Dietrich, 2021; Brooks, Hoberg, et al., 2022; Trivellone, Cao, et al., 2022; Trivellone, Hoberg, et al., 2022). Cultural transformation is conceptual and operational, serving to build and expand a permanent/sustainable infrastructure around biorepositories rather than perpetuating business-as-usual in cycles of partitioned research networks (Figures 1 and 2).

A new model and long-term commitments are required for natural history collections to effectively serve informatics resources (inextricably tied to the specimens in their archives) and actionable information. Collections codify a cumulative view across the interconnected arena of pathogens, hosts, reservoirs, vectors, and interfaces through targeted, site-intensive, and geographically extensive

explorations of diversity examined in the context of phylogenetic triage, which will help us establish the limits of risk space (Hoberg, Boeger, Brooks, et al., 2022). A new model encompasses building or extending infrastructure for personnel, facilities, and capacities, especially in biodiverse regions of our planet. Pathogens are a component of broader global diversity; thus to be effective, new trajectories should be in parallel and revitalize (unrealized) expansions of the systematics/phylogenetics/biodiversity community proposed more than two decades ago (e.g., in part summarized in Brooks and Hoberg, 2001). New capacities and policies should also reflect recent calls for expansion of surveillance (but, ironically, biorepositories have not been central to these proposals) in response to emergent public health crises (Alimi et al., 2021; Holmes, 2022). Some components are best achieved on large scales, including global archives and information storage with broad accessibility, supported and coordinated at national and international levels. Appropriately, such commitments require direct governmental infrastructure, cooperation, and new official capacities that recognize and codify EID as a priority across national and international boundaries (Brooks et al., 2019). A critical aspect going forward has been succinctly outlined by Colella et al. (2021):

*Biodiversity data portals have been implemented at very large scales with >225 million specimens (approximately 31 million of which belong to Chordata) digitized worldwide (gbif.org, accessed January 5, 2021), but these data must be quality checked and updated regularly and enriched via standardization of key fields, such as reproductive status, age, sex, geographic coordinates, etc. Trained personnel are essential to ensuring databases are kept accurate and up to date. Examples of digital biodiversity databases include the Global Biodiversity Information Facility (GBIF; gbif.org), VertNet (vertnet.org), iDigBio (idigbio.org), the Sistema de Inforcação Sobre a Biodiversidade Brasileira (SiBBR; sibbr.gov.br), the Global Genome Biodiversity Network (GGBN; ggbn.org), and speciesLink (splink.cria.org.br).*

Other facets will require incremental implementation on a place-by-place basis according to local needs and capacity. In synergy, building on existing collections-oriented networks across scales, broader capacity can be augmented and achieved (e.g., Colella et al., 2021). In an absence of a unified culture that values specimens, archives, and collections, we will be challenged to understand the limits of diversity, evolution, and biogeography and will be

circumscribed in our abilities to develop integrated, temporal, and spatial snapshots of the world that become critical baselines. As a global and globalized community, it is essential to abandon business as usual while looking forward toward increasingly transboundary approaches that maximize a proactive stance, extending our conceptual and taxonomic view of diversity across interconnected planetary scales that influence the complexity of pathogen-host interfaces (Hoberg et al., 2015; Brooks et al., 2019). The dimensions of the SP with an evolutionary/historical perspective and the DAMA protocol with collections and specimens as an extended empirical foundation reveal a broad, inclusive vision and the necessity for a transformation of the One Health arena.

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